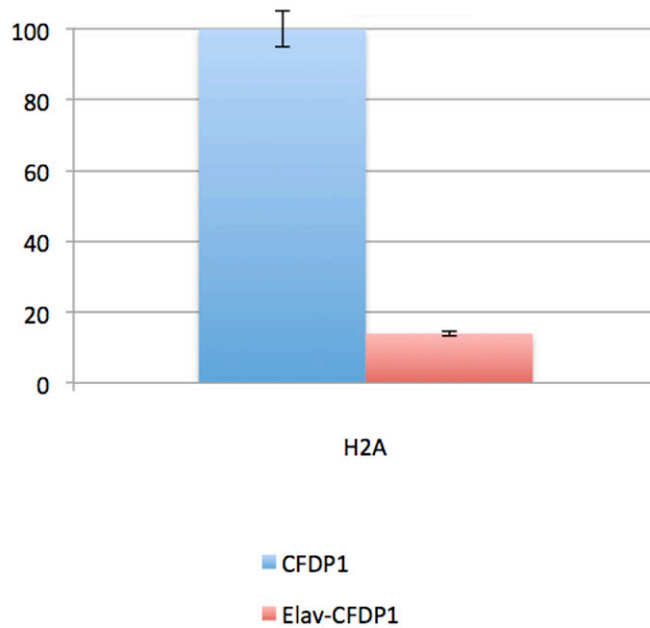
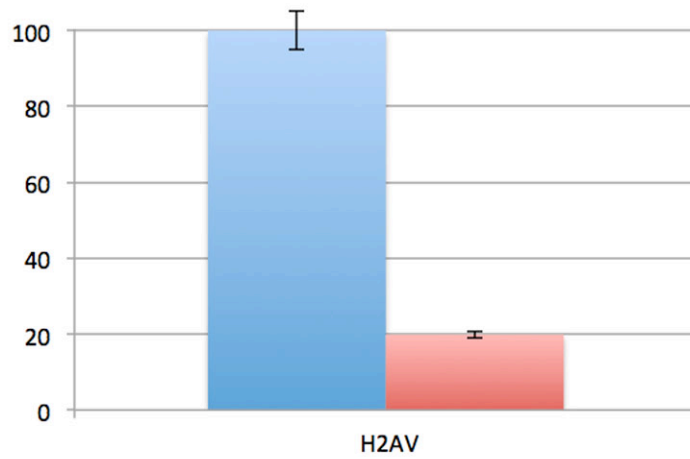


## Supplementary figures

Expression of human *Cfdp1* gene in *Drosophila* reveals new insights into the function of the evolutionarily conserved BCNT protein family

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Patrizio Dimitri



**Supplementary Figure 1** Measurements of fluorescence levels of H2A.V and H2A on polytene chromosomes

About 80 and 85% decrease in levels of H2A.V and H2A, respectively, occurs in *elav-GAL4<sup>[w+]</sup>/w;UAS-Cfdp1<sup>[w+]</sup>/+* compared to *UAS-Cfdp1<sup>[w+]</sup>/UAS-Cfdp1<sup>[w+]</sup>* controls. Measurements of polytene chromosome fluorescence levels of H2A.V and H2A were performed using the ImageJ software.

## YETI



## CFDP1

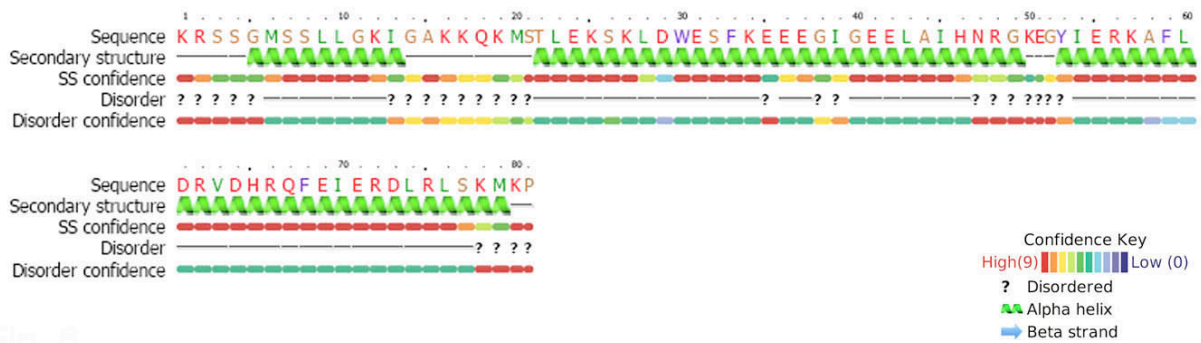


Fig. 8

### Supplementary Figure 2 Secondary structure analysis of BCNT domain between YETI and CFDP1

The secondary structure analysis of YETI and CFDP1, performed using the Phyre2 algorithm, predict  $\alpha$ -helix stretches in the C-terminal BCNT domain of YETI (residues 181-237) and CFDP1. The  $\alpha$ -helical coiled coil is the simplest of all protein-protein interaction motifs and consists of two or more  $\alpha$ -helices that wrap around each other with a super-helical twist.